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Phenotypic and genotypic characteristics of *Listeria monocytogenes* strains isolated during 2011-2014 from different food matrices in Switzerland

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Contents

Phenotypic and genotypic characteristics of *Listeria monocytogenes* strains isolated during 2011-2014 from different food matrices in Switzerland

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Running title: Characterization of food *L. monocytogenes* strains

Keywords: *Listeria monocytogenes*; food; serotype; MLST

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1. Abstract / Zusammenfassung

Abstract: One hundred and forty two *L. monocytogenes* strains isolated from different food matrices in Switzerland between 2011 and 2014 were characterized with respect to their genotypic and phenotypic properties. Analyzed strains originated from various meat, milk, plant-associated food products and production environments as well as from other types of foods including fish, seafood, and ready to eat (RTE) products. The collection included serotype 1/2a (64%), 4b (15%), 1/2c (12%), 1/2b (7%) and 3c (3%). The strains were genetically diverse representing 61 MLST sequence types (ST) including 24 new STs. The most frequent clonal complexes (CC) were CC9 (15%) and CC121 (12%). PCR screening detected presence of the stress survival islet (SSI-1) in 50 % of the strains. Phenotypic resistance to benzalkonium chloride (BC) was detected in 18% of the strains. The BC resistance genetic determinants *qacH* and *bcrABC* were detected in 80% and 12% of the strains, respectively. Most (n=129) of the strains isolated from Swiss food matrices exhibited poor biofilm formation capacity and there were no correlations detected between strain serotypes, genotypes and biofilm production.

Keywords: *Listeria monocytogenes*; food; serotype; MLST

Zusammenfassung: Hundertzweiundvierzig aus verschiedenen Lebensmitteln stammende L. monocytogenes Stämme wurden zwischen 2011 und 2014 isoliert und im Zuge dieser Arbeit aufgrund von phänotypischen und genotypischen Eigenschaften charakterisiert. Der Ursprung der Isolate liegt in fleisch-, milch- und pflanzenassoziierten Lebensmitteln und deren Produktionsumfeld sowie anderen Lebensmittelklassen wie Fisch, Meeresfrüchte und Fertiggerichte. Das Stammkollektiv beinhaltet die Serotypen 1/2a (64 %), 4b (15 %), 1/2c (12 %), 1/2b (7 %) und 3c (3 %). Die Stämme repräsentierten 61 MLST Sequenz Typen (ST), wovon 24 neu beschrieben wurden. Die häufigsten Klonalen Komplexe (CC) waren CC9 (15 %) und CC121 (12 %). PCR Analysen ergaben, dass 50 % der Stämme Träger der stress survival islet (SSI-1) sind. Eine phänotypische Benzalkoniumchloridresistenz (BC) konnte in 18 % der Stämme nachgewiesen werden. Die genetischen BC Resistenz Determinanten qacH und bcrABC wurden in 80 % beziehungsweise 12 % dieser Stämme gefunden. Der Grossteil (n=129) der Stämme wies

geringe Biofilmkapazität auf. Zudem konnte keinerlei Korrelation zwischen den Serotypen, den Genotypen und der Biofilmproduktion gefunden werden.

Schlüsselwörter: Listeria monocytogenes; Lebensmittel, Serotyp; MLST

2. Introduction

Listeria monocytogenes is an important foodborne pathogen with a significant impact on public health and economy worldwide. Although human infections with *L. monocytogenes* occur rarely they lead in those with diminished immunity to serious and life-threatening disease conditions (listeriosis) including septicemia, meningitis, meningoencephalitis and abortion (Dogany, 2003). Because of its high case fatality rate, listeriosis ranks among the most frequent causes of death due to foodborne illnesses (Anonymous, 2009). In the European Union there were 1,476 confirmed cases of listeriosis reported in 2011 resulting in an overall notification rate of 0.32 cases per 100,000 people (Anonymous, 2013a). In Switzerland, the annual incidence over the past ten years ranged from 0.47 to 1.22 cases per 100,000 people. So far, four bigger Swiss listeriosis outbreaks have occurred including the latest one in 2013/2014 caused by contaminated ready-to-eat salad (Bula et al., 1995; Bille et al., 2006; Haechler et al., 2013; Stephan et al., 2015). Althaus et al. (2013) recently characterized *L. monocytogenes* strains from human listeriosis cases that occurred in Switzerland during the period 2011-2013.

Biofilm formation and resistance to disinfectants (e.g. benzalkonium chloride [BC]) are among phenotypic factors attributed to survival and persistence of *L. monocytogenes* in food associated environments from where they can be transferred to food leading to contamination (Moretro and Langsrud, 2004; Soumet et al., 2005; Mullapudi et al., 2008). Furthermore, genes comprising the stress survival islet (SSI-1) have been shown to promote growth and survival of *L. monocytogenes* under food-associated stress conditions (Ryan et al., 2010). Knowledge about the distribution of genetic elements such as SSI-1 and the phenotypic capacity to form biofilm and resist to BC amongst food-associated *L. monocytogenes* strains is therefore important.

3. Material and Methods

3.1. Strain selection

One hundred and forty two *L. monocytogenes* strains collected between 2011 and 2014 by the Swiss National Reference Centre for Enteropathogenic Bacteria and Listeria were characterized. This strain collection comprises isolates that were collected through elective *L. monocytogenes* screenings performed by food processing companies as well as those collected in the course of periodical inspections undertaken by the authorities.

3.2. Phenotypic characterization

Strains serotypes were determined using the commercial set of Listeria O-factor and H-factor antisera from Denka Seiken (Pharma Consulting, Burgdorf, Switzerland) according to the manufacturer's instructions. BC resistance was determined as previously described (Mullapudi et al., 2008). Briefly, overnight cultures from each strain grown in Mueller Hinton (MH) broth were spotted and incubated 48 hrs at 37°C on MH agar plates (Oxoid, Pratteln, Switzerland) with 2 % defibrinated sheep blood (Oxoid, Pratteln, Switzerland) and supplemented with different BC concentrations (0, 5, 10, 15, 20, 25, 30, 35, and 40 □g/ml). Biofilm formation capacity of the strains was assessed in Tryptone Soy Broth (TSB; Oxoid, Pratteln, Switzerland) media using the crystal violet staining method in microtitre plates as previously described by Harvey et al. (2007). Briefly, overnight cultures prepared from each strain were inoculated in triplicate on 96 well microtitre plates that included 9 control wells containing 100 □l of un-inoculated TSB (Thermo Fisher Scientific, Roskilde, Denmark) and incubated at 20 °C for 48 h. The formed biofilms were subsequently stained using 1% crystal violet solution and quantified by measuring optical density at 595 nm.

3.3. Genotypic characterization

Multi locus sequence typing (MLST) was performed as described by Ragon et al. (2008) and the alleles and sequence types (STs) determined are publicly available at http://www.pasteur.fr/mlst. PCRs to determine the presence of the five genes comprising the stress survival islet (*lmo0444-lmo0448*) were performed using the primers described by Ryan et al. (2010) and the Phusion High Fidelity Taq Polymerase system (Thermoscientific, St. Leon-Rot, Germany). PCRs to determine *qacH* and *bcrABC* presence were conducted

using primers described by Müller et al. (2013) and Elhanafi et al. (2010), respectively, and the Go Taq Green Master Mix (Promega, Madison, USA).

4. Results

Overall strains from serotypes 1/2a (n=91) and 4b (n=21) were the most frequently isolated, whereas serotypes 1/2b, 1/2c and 3c were found at lower frequency (Table 1). Among the meat-associated isolates serotypes 1/2a (n=52), 1/2b (n=6), 1/2c (n=15), 3c (n=3) and 4b (n=13) were represented. Serotypes 1/2a (n=24), 1/2b (n=3), 1/2c (n=1) and 4b (n=6) were found among strains recovered from milk-associated products. Strains from plant associated food products comprised serotypes1/2a (n=6), 1/2c (n=1) and 4b (n=2). Serotypes 1/2a (n=9) and 1/2b (n=1) were the only serotypes found among strains derived from other food products.

Using MLST there were 61 different sequence types (ST) detected among the 142 *L. monocytogenes* strains analyzed including 24 newly assigned STs: ST 724 – 728, 733 and 738 – 755. The 61 STs were grouped into 24 clonal complexes (CC) and 6 singletons (Figure 1; Table 2). ST9 (n=18) and ST121 (n=14) formed the most frequent STs. ST2 and ST204 comprised seven strains, ST155 six strains, ST6 and ST8 five strains, ST3 and ST504 four strains and ST16, ST230, ST415 and ST415 three strains. The rest of the STs were all represented by either two or one strains. The MLST data of the food strains was compared with previously published MLST data from clinical Swiss strains (Althaus et al., 2014) and previous MLST studies (Ragon et al., 2008; Chenal et al., 2011; Cantinellli et al., 2013; Chenal et al., 2013; Haase et al., 2014). The observed diversity represented a large fraction of the known diversity of clones of *L. monocytogenes* (Figure S1). ST9 included serotype 1/2c (n=13), 1/2a (n=3) and 3c (n=2) strains; ST121 1/2a (n=13) and 3c (n=1) strains and ST155 serotype 1/2a (n=5) and 1/2c (n=1) strains. Other STs that also contained more than one strain all comprised of a single serotype. Apart from serotype 1/2c, which was isolated more often from meat associated products than others there was no significant correlation found between genetic lineage, serotype or clonal complex and the matrix origin of the strains.

The SSI-1 was detected in 50% (71/142) of the strains representing a variety of MLST sequence types (Table S1). In general all strains within a given CC either harbored or lacked SSI-1. An exception to this observation was only detected within CC9 where one strain was SSI-1 negative. In 5 serotype 1/2a strains assigned to ST748, ST451, ST9, ST307 and ST738, the SSI-1 PCR primers failed to amplify. In these strains the 9.7 kb or 1.1 kb PCR amplicons expected for SSI-1 positive and negative strains, respectively, were not observed. Additionally there were 21 serotype 1/2a strains representing ST20, ST121, ST504, ST741, ST749, and ST755 that showed 2.2 kb amplicons consistent with such strains harboring homologs to *L. innocua* genes (*lin0464* and *lin0465*) instead of the five genes comprising the *L. monocytogenes* SSI-1 genes. These results confirm the dynamics of integration of different gene clusters at this genome location.

Resistance to BC was detected in 18% (25/142) of the strains that showed growth at BC concentration of ≥ 10 µg/ml. These strains showed MICs of 10 µg/ml (n=3), 15 µg/ml (n=3), 20 µg/ml (n=4), 25 µg/ml (n=10) and 30 µg/ml (n=5). PCR analysis showed 20 (80%) and 3 (12%) of these strains to harbor *qacH* and *bcrABC*, respectively, whereas these BC resistance determinants were not detected in 2 (8%) of the BC resistant strains (Table S1). BC resistant strains were distributed between five MLST CC and one singleton. Strains from CC9 (n=2), CC20 (n=1), CC31 (n=1), CC121 (n=15) and ST749 (n=1) harbored *qacH*, whereas *bcrABC* was harbored by strains from CC9 (n=2) and CC31 (n=1). The remaining two BC resistant strains belonged to CC31 (n=1) and CC504 (n=1).

One hundred and twenty nine (91%) strains were classified as poor (CV OD_{595} < 0.2), 11 (8%) as medium (CV OD_{595} range 0.2 – 0.35) and 2 (1%) as high (CV OD_{595} > 0.5) biofilm formers. Strains classified as medium and high biofilm formers represented various serotypes and genotypes. Overall there was no correlation detected between biofilm formation capacity and strain serotype, genotype or isolation source.

5. Discussion

Similar to other countries around the world listeriosis remains a significant public health and food safety threat in Switzerland. Food products are the primary source for human infection and an improved understanding of the distribution and characteristics of food associated *L. monocytogenes* is necessary in order to improve our understanding of the potential threat and contribution of various food matrices to human listeriosis transmission. In this study we have characterized 142 *L. monocytogenes* strains that were isolated from different food matrices including meat (63%), milk (24%) and vegetables (6%) food products and their associated production environments as well as from other (7%) food categories in Switzerland during the time period from 2011 to 2014.

Serotype distribution analysis among these strains revealed that 1/2a was the most prevalent serotype. These observations are in agreement with various previous studies from other countries, (Gianfranceschi et al., 2009; Parisi et al., 2010; Kramarenk et al., 2013; Martín et al., 2014). In contrast to serotypes 1/2a, 1/2b and 4b that were more evenly distributed among strains recovered from the different food sources examined, the serotype 1/2c strains showed a bias towards meat association. Similar observations have been previously reported by others (Gianfranceschi et al., 2009; Kramarenk et al., 2013; Martín et al., 2014).

MLST genotyping grouped the strains into 61 STs that were assigned to 24 clonal complexes and 6 singletons. Genetic lineages assignment showed that lineage II (78% vs 22%) was more prevalent compared to lineage I among the Swiss food associated *L. monocytogenes* strains isolated during this period. These observations are similar to those reported from several other countries showing that lineage II strains are more frequently isolated from food and food associated environments compared to those of lineage I (Autio et al., 2002; Gianfranceschi et al., 2009; Parisi et al. 2010; Kramarenk et al., 2013; Haase et al., 2014; Martín et al., 2014). MLST analysis also showed a high prevalence of CC9 and CC121 in the food associated *L. monocytogenes* isolates in Switzerland. These observations are in agreement with those reported by Chenal-Francisque et al. (2011) who described a frequent appearance of these two clonal complexes in many countries. In addition, Parisi et

al. (2010) and Martín et al. (2014) have also reported a wide occurrence of ST9 and ST121 in meat-processing environments.

PCR based analysis of the 142 strains showed a 50% SSI-1 prevalence among the examined Swiss strains. In agreement with previous reports the SSI-1 in these strains is harboured by non-serogroup 4 strains that mostly belong to genetic lineage II (56.8 %) (Ryan et al., 2010; Hein et al., 2011; Arguedas-Villa et al., 2014). A subset of ST112 serotype 1/2a *L. monocytogenes* strains that amplify smaller SSI-1 amplicons (2.2 kb instead of 9.2 kb) because they harbour homologs of *L. innocua* genes *lin0464* and *lin0465* instead of the *L. monocytogenes* SSI-1 gene set were previously also reported (Hein et al., 2011; Arguedas-Villa et al., 2014). A similar subset was detected in the current study. But in addition to ST 121 strains, this subset also includes serotype 1/2a strains that belong to ST20, ST504, ST741, ST749, and ST755.

Previous studies have documented BC resistance among *L. monocytogenes* strains isolated in various countries (Mullapudi et al., 2008; Ratani et al., 2012; Dutta et al., 2013; Xu et al., 2014). Among Swiss *L. monocytogenes* strains analyzed here a BC resistance prevalence of 18% (25/142) was determined. All BC resistant strains detected here belonged to genetic lineage II although other studies have detected BC resistance in both genetic lineage I and II strains (Mullapudi et al., 2008; Ratani et al., 2012; Dutta et al., 2013; Xu et al., 2014). Most of the BC resistance strains detected possessed *qacH* (80%) and *bcrABC* (12%), whereas 8% (2/25) did not harbour either of these two BC resistance determinants. Müller at al. (2013) in their previous study also reported both *qacH* and *bcrABC* harboring BC resistant *L. monocytogenes* strains in their strain collection. Interestingly four CC9 strains resistant to BC were divided into two serotypes. One group harbored *qacH* and belonged to serotype 3c, whilst the other group harbored *bcrABC* and belonged to serotype 1/2c. Similar to our observations, BC resistant *L. monocytogenes* strains lacking known resistance determinants such as *qacH* or *brcABC* have been previously observed (Ortiz et al., 2014). Possible explanations put foward for the increased BC tolerance in such strains include a mutation in endogenous efflux pumps (Romanova et al., 2006; Rakic-Martinez et al., 2011) or modifications in the cell wall that somehow reduce BC access to its cell membrane target (To et al., 2002).

Assessment of biofilm formation capacity revealed that the majority of the strains isolated from the different food matrices are poor biofilm formers. There were, however, a few strains that displayed medium to strong biofilm formation tendency. These findings are similar to those reported by other authors (Harvey et al., 2007; Barbosa et al., 2013; Guilbaud et al., 2014). Similar to Harvey et al. (2007) there were no difference in biofilm production capacity detected between strains derived from different food sources and associated production environments. Furthermore no relationship could be discerned between biofilm formation and strain serotypes or MLST genotypes.

Strains that caused human listeriosis between 2011 and 2013 in Switzerland were recently characterized showing that serotypes 1/2a (62.4 %), 1/2b (5.4 %), 1/2c (2.1 %) and 4b (30.1 %) strains were associated with human infections during this time period (Althaus et al., 2014). In comparison to the current study that characterized *L. monocytogenes* strains associated with different food matrices sampled in an overlapping time period there was a similar high prevalence of serotype 1/2a and 4b strains reflected in food products and the human listeriosis cases. A comparison based on MLST genotypes showed genetically diverse and overlapping *L. monocytogenes* populations among Swiss clinical cases and food associated strains. However there were differences in the predominating genotypes. Although ST9 (n=18) and ST121 (n=14) were the most frequent among food isolates they were significantly less frequent among the human listeriosis isolates. In contrast ST1 and ST8 were the most prevalent sequence types in the human strains collection but rare among food isolates (Figure 1).

6. Conclusion

The present study delivers insights into the genetic and phenotypic characteristics of food derived *L. monocytogenes* strains occurring in Switzerland. No links between serotypes, lineages or MLST types on the one hand, and the food type of origin of the strains on the other hand, were found. The MLST sequence types found in Switzerland are largely distributed across the global clonal diversity of *L. monocytogenes*. The results further highlight strain differences in the occurrence of several genetic elements, which are linked to bacterial persistence.

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8. Tables

Tab. 1

Distribution of *L. monocytogenes* strains and serotypes between different food matrices

Serotype	Overall	Meat associated	Milk associated	Plant associated	Others
1/2a	64 % (91)	58 % (52)	71 % (24)	67 % (6)	90 % (9)
1/2b	7 % (10)	7 % (6)	9 % (3)		10 % (1)
1/2c	12 % (17)	17% (15)	3 % (1)	11 % (1)	
3c	2 % (3)	3 % (3)			
4b	15 % (21)	15 % (13)	18 % (6/34)	22 % (2)	
Total	142	89	34	9	10

Tab. 2

Distribution of Clonal complex between different food matrices

Clonal Complex	ST	Overall	Meat associated	Milk associated	Plant associated	Others
CC1		**4**				
	ST1		0	2	0	0
	ST727		1	0	0	0
	ST746		1	0	0	0
CC2		**8**				
	ST2		6	1	0	0
	ST724		1	0	0	0
CC3		**4**				
	ST3		1	3	0	0
CC4		**2**				
	ST4		1	0	1	0
CC5		**3**				
	ST5		2	0	0	0
	ST745		1	0	0	0
CC6		**5**				
	ST6		3	2	0	0
CC7		**4**				
	ST7		1	0	0	1
	ST158		1	0	0	0
	ST752		1	0	0	0
CC8		**10**				
	ST8		3	1	0	1
	ST15		0	2	1	0
	ST742		1	0	0	0
	ST743		1	0	0	0
CC9		**21**				
	ST9		13	4	1	0
	ST477		1	0	0	0
	ST751		1	0	0	0
	ST753		1	0	0	0
CC14		**3**				
	ST91		1	1	0	0
	ST726		0	1	0	0
CC20		**2**				
	ST20		0	0	1	1
CC21		**3**				
	ST21		0	2	0	0
	ST725		1	0	0	0
CC26		**4**				
	ST26		0	0	1	0
	ST501		1	0	0	0

ST750		0	1	0	0
ST754		1	0	0	0
CC29	**1**				
ST29		0	1	0	0
CC31	**5**				
ST31		2	0	0	0
ST725		0	2	0	0
ST748		0	1	0	0
CC37	**4**				
ST37		2	0	0	0
ST728		1	0	0	0
ST747		1	0	0	0
CC59	**2**				
ST59		2	0	0	0
CC101	**1**				
ST101		1	0	0	0
CC121	**17**				
ST108		1	0	0	0
ST121		12	0	1	1
ST741		1	0	0	0
ST755		0	1	0	0
CC155	**6**				
ST155		6	0	0	0
CC177	**1**				
ST740		0	1	0	0
CC199	**3**				
ST230		0	3	0	0
CC204	**7**				
ST204		6	0	0	1
CC361	**4**				
ST415		3	0	0	0
ST744		0	1	0	0
CC403	**1**				
ST738		1	0	0	0
CC451	**2**				
ST451		1	0	0	0
ST733		1	0	0	0
CC504	**4**				
ST504		0	0	0	4
Singleton 36	**3**	2	1	0	0
Singleton 217	**2**	0	1	1	0
Singleton 226	**1**	0	0	1	0
Singleton 307	**1**	0	1	0	0
Singleton 375	**1**	0	0	1	0
Singleton 517	**1**	0	0	0	1
Singleton 739	**1**	1	0	0	0
Singleton 749	**1**	1	0	0	0

9. Figures

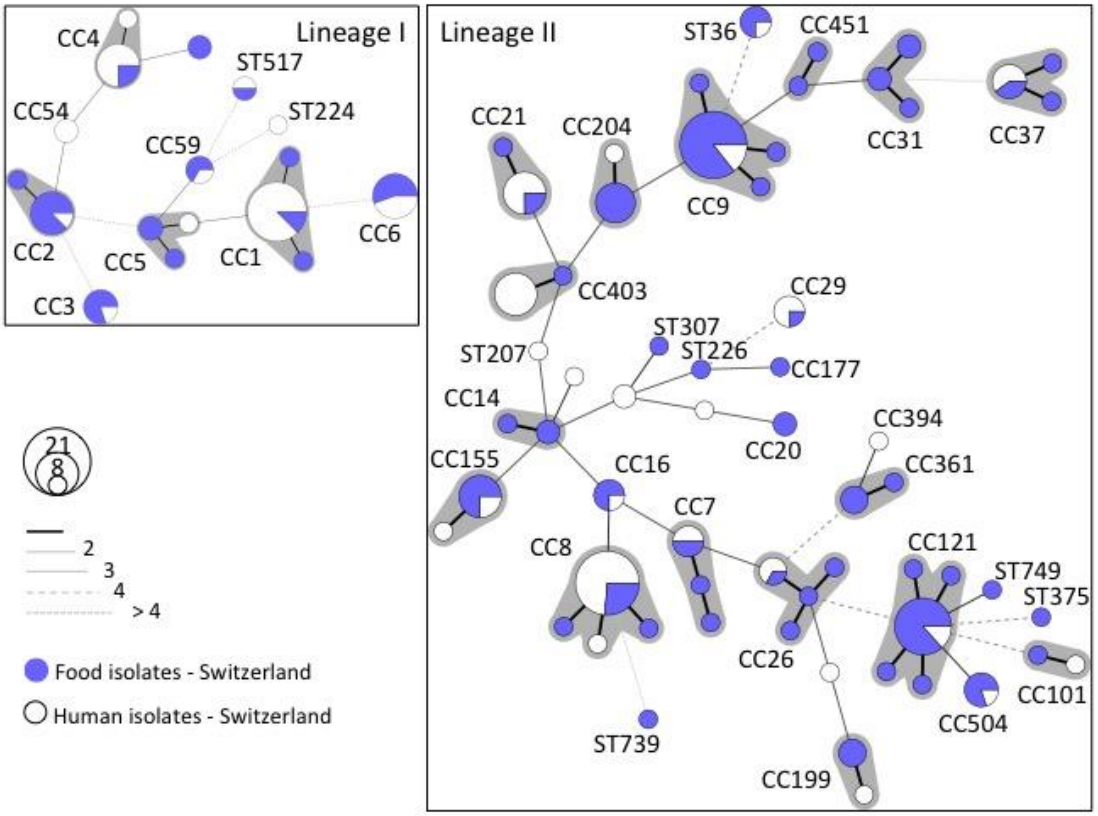

Fig. 1

Minimum spanning tree of MLST data for 235 *L. monocytogenes* strains originating from Switzerland. Each circle is representing a ST, circle size correlates to the number of strains within the same ST. CC are illustrated by the grey zones surrounding different circles. Blue segments represent the 142 *L. monocytogenes* strains associated with food from this study, white segments represent 93 *L. monocytogenes* previously published by Althaus et al. (2014) linked to human listeriosis cases in Switzerland.

10. Supplementary documents

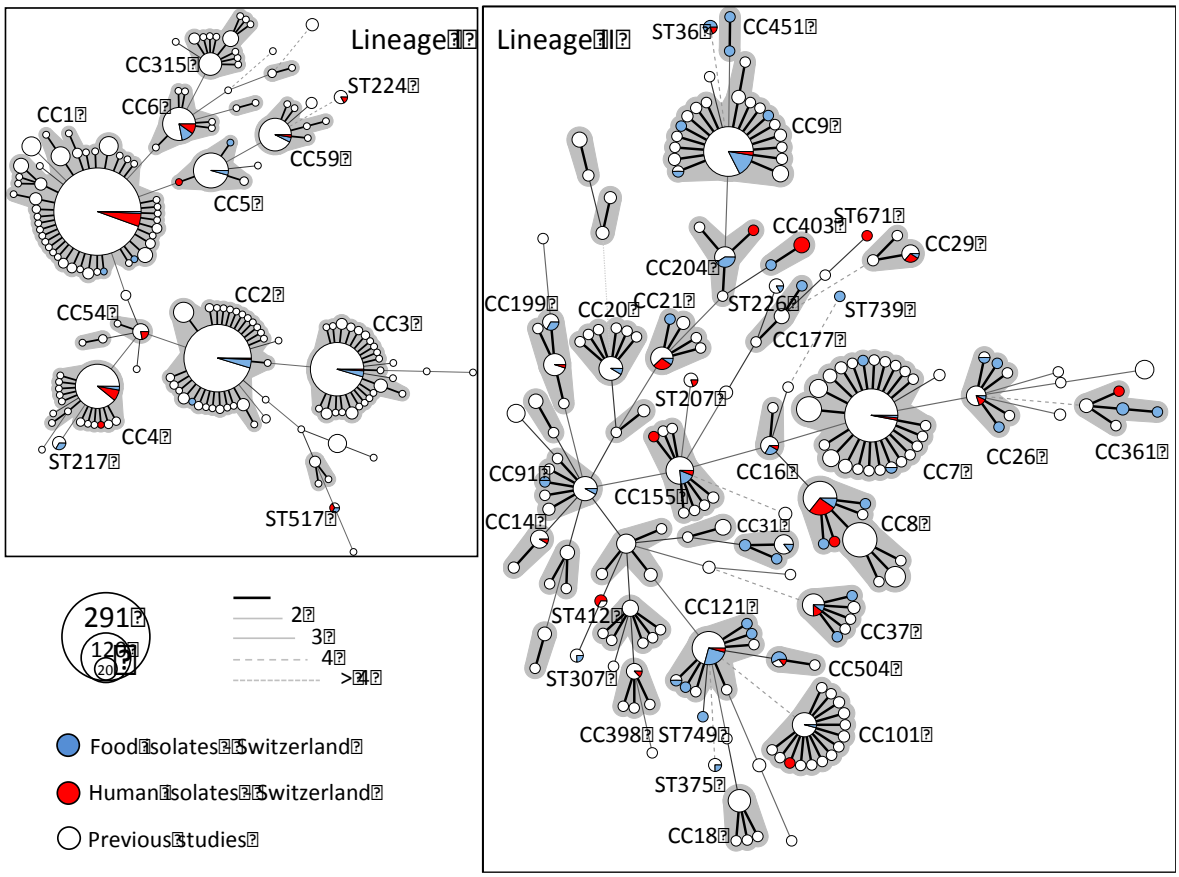

Fig. S1

Minimum spanning tree of MLST data for 1098 *L. monocytogenes* strains. Blue segments represent the 142 *L. monocytogenes* strains from this study, red segments represent 93 *L. monocytogenes* previously published by Althaus et al. (2014) linked to human listeriosis cases in Switzerland and white segment represent other previously published strains (Ragon et al., 2008; Chenal-Francisque et al., 2011; Cantinelli et al., 2013; Chenal-Francisque et al., 2013).

Tab. S1

Characteristics of the 142 strains included in the study

Strain No.	Lineage	Clonal Complex	Sequence Type	Year	Source	Serotype	Phenotypic Benzalkonium Tolerance[a] [µg/ml]	PCR Result		Biofilm formation measured at OD595	SSI-1
								TN6188	*bcrABC*		
98	I	CC1	1	2012	cheese environment	4b		-	-	0.03	-
127	I	CC1	1	2013	milk	4b		-	-	0.00	-
55	I	CC1	727	2012	raw sausage	4b		-	-	0.03	-
74	I	CC1	746	2012	meat	4b		-	-	0.15	-
18	I	CC2	2	2011	meat	4b		-	-	0.05	-
35	I	CC2	2	2012	meat	4b		-	-	0.01	-
42	I	CC2	2	2012	meat	4b		-	-	0.00	-
47	I	CC2	2	2012	meat	4b		-	-	0.00	-
49	I	CC2	2	2012	meat	4b		-	-	0.00	-
67	I	CC2	2	2012	meat product	4b		-	-	0.08	-
165	I	CC2	2	2013	smear water of cheese	4b		-	-	0.01	-
12	I	CC2	724	2011	meat	4b		-	-	0.13	-
53	I	CC3	3	2012	cheese environment	1/2b		-	-	0.17	+
69	I	CC3	3	2012	meat	1/2b		-	-	0.16	+
125	I	CC3	3	2012	cheese environment	1/2b		-	-	0.14	+
211	I	CC3	3	2014	cheese crust	1/2b		-	-	0.06	+
170	I	CC4	4	2013	meat	4b		-	-	0.04	-
229	I	CC4	4	2014	vegetables environment	4b		-	-	0.00	-
136	I	CC5	5	2013	meat	1/2b		-	-	0.07	+
163	I	CC5	5	2013	poultry	1/2b		-	-	0.02	+

68	I	CC5	745	2012	meat	1/2b	-	-	0.06	+
45	I	CC6	6	2012	food enviroment	4b	-	-	0.03	-
87	I	CC6	6	2012	milk	4b	-	-	0.03	-
143	I	CC6	6	2013	milk	4b	-	-	0.01	-
154	I	CC6	6	2013	meat	4b	-	-	0.02	-
227	I	CC6	6	2014	meat environment	4b	-	-	0.03	-
2	I	CC59	59	2011	raw sausage	1/2b	-	-	0.04	-
73	I	CC59	59	2012	meat	1/2b	-	-	0.25	-
15	I	ST217	217	2011	smear water of cheese	4b	-	-	0.84	-
82	I	ST217	217	2012	vegetables environment	4b	-	-	0.05	-
3	I	ST517	517	2011	noodle salad	1/2b	-	-	0.11	+
63	II	CC7	7	2012	meat product	1/2a	-	-	0.06	+
75	II	CC7	7	2012	ready to eat product	1/2a	-	-	0.06	+
60	II	CC7	158	2012	meat	1/2a	-	-	0.10	+
57	II	CC7	752	2012	scaleded sausage	1/2a	-	-	0.11	+
6	II	CC8	8	2011	meat	1/2a	-	-	0.06	+
10	II	CC8	8	2011	ham product	1/2a	-	-	0.17	+
16	II	CC8	8	2011	cheese	1/2a	-	-	0.09	+
31	II	CC8	8	2012	seafood	1/2a	-	-	0.06	+
219	II	CC8	8	2014	meat environment	1/2a	-	-	0.13	+
22	II	CC8	16	2011	milk product	1/2a	-	-	0.23	+
86	II	CC8	16	2012	vegetables environment	1/2a	-	-	0.04	+
168	II	CC8	16	2013	milk	1/2a	-	-	0.08	+
8	II	CC8	742	2011	meat	1/2a	-	-	0.02	+

7	II	CC8	743	2011	meat	1/2a		-	-	0.14	+
4	II	CC9	9	2011	meat	1/2c		-	-	0.13	+
9	II	CC9	9	2011	meat	1/2c		-	-	0.24	+
14	II	CC9	9	2011	meat	1/2c		-	-	0.58	+
33	II	CC9	9	2012	smear water of cheese	1/2a		-	-	0.04	+
34	II	CC9	9	2012	milk product	1/2a		-	-	0.08	+
51	II	CC9	9	2012	milk	1/2c		-	-	0.09	+
52	II	CC9	9	2012	meat	1/2c		-	-	0.08	+
56	II	CC9	9	2012	meat	1/2c	25	-	+	0.07	+
88	II	CC9	9	2012	meat	1/2c		-	-	0.13	-
92	II	CC9	9	2012	milk product	1/2a		-	-	0.10	nd
97	II	CC9	9	2012	rice	1/2c		-	-	0.15	+
155	II	CC9	9	2013	meat	1/2c		-	-	0.08	+
164	II	CC9	9	2013	poultry	1/2c		-	-	0.05	+
185	II	CC9	9	2014	dryed meat	1/2c		-	-	0.07	+
204	II	CC9	9	2014	dryed meat	1/2c		-	-	0.03	+
216	II	CC9	9	2014	meat environment	1/2c		-	-	0.15	+
225	II	CC9	9	2014	meat environment	3c	10	+	-	0.01	+
226	II	CC9	9	2014	meat environment	3c	10	+	-	0.03	+
58	II	CC9	477	2012	meat	1/2c		-	-	0.08	+
64	II	CC9	751	2012	poultry	1/2c		-	-	0.16	+
61	II	CC9	753	2012	meat	1/2c	25	-	+	0.08	+
130	II	CC14	91	2013	raw sausage	1/2a		-	-	0.06	-
139	II	CC14	91	2013	cheese environment	1/2a		-	-	0.05	-

36	II	CC14	726	2012	milk	1/2a		-	-	0.03	-
21	II	CC20	20	2011	mixed salad	1/2a		-	-	0.07	-
25	II	CC20	20	2011	salmon	1/2a	30	+	-	0.31	*
76	II	CC21	21	2012	milk product	1/2a		-	-	0.11	-
166	II	CC21	21	2013	milk	1/2a		-	-	0.00	-
24	II	CC21	725	2011	meat	1/2a		-	-	0.12	-
65	II	CC26	26	2012	vegetabels	1/2a		-	-	0.18	+
59	II	CC26	501	2012	meat	1/2a		-	-	0.11	+
79	II	CC26	750	2012	milk product	1/2a		-	-	0.10	+
50	II	CC26	754	2012	cheese enviroment	1/2a		-	-	0.08	+
5	II	CC29	29	2011	milk	1/2a		-	-	0.07	-
172	II	CC31	31	2013	sausage	1/2a	15	+	-	0.15	+
239	II	CC31	31	2005	meat product	1/2a	10	-	-	0.07	+
132	II	CC31	325	2013	milk	1/2a		-	-	0.00	+
135	II	CC31	325	2013	milk	1/2a	20	-	+	0.00	+
129	II	CC31	748	2013	milk	1/2a		-	-	0.00	nd
11	II	ST36	36	2011	milk product	1/2a		-	-	0.15	+
138	II	ST36	36	2013	meat	1/2a		-	-	0.02	+
142	II	ST36	36	2013	meat	1/2a		-	-	0.16	+
84	II	CC37	37	2012	meat	1/2a		-	-	0.01	-
214	II	CC37	37	2014	steak tartar	1/2a		-	-	0.06	-
26	II	CC37	728	2011	meat	1/2a		-	-	0.12	-
77	II	CC37	747	2012	meat	1/2a		-	-	0.03	-
128	II	CC101	101	2013	meat	1/2a		-	-	0.05	-

1	II	CC121	108	2011	poultry	1/2a	25	+	-	0.27	*[b]
23	II	CC121	121	2011	corn	1/2a		-	-	0.16	-
38	II	CC121	121	2012	quorn	1/2a	25	+	-	0.10	*
43	II	CC121	121	2012	meat	1/2a	20	+	-	0.18	*
48	II	CC121	121	2012	meat	1/2a	15	+	-	0.11	*
72	II	CC121	121	2012	meat	1/2a		-	-	0.15	*
78	II	CC121	121	2012	meat	1/2a	25	+	-	0.24	*
134	II	CC121	121	2013	meat	1/2a	25	+	-	0.06	*
144	II	CC121	121	2013	meat	1/2a	25	+	-	0.11	*
147	II	CC121	121	2013	meat	1/2a	25	+	-	0.14	*
159	II	CC121	121	2013	meat	1/2a	30	+	-	0.05	*
162	II	CC121	121	2013	meat	1/2a	25	+	-	0.05	*
169	II	CC121	121	2013	foie gras	1/2a	15	+	-	0.27	*
182	II	CC121	121	2014	meat	1/2a	25	+	-	0.11	*
196	II	CC121	121	2014	meat environment	3c	20	+	-	0.20	-
19	II	CC121	741	2011	poultry	1/2a	30	+	-	0.16	*
54	II	CC121	755	2012	meat	1/2a	25	+	-	0.07	*
156	II	CC155	155	2013	meat	1/2a		-	-	0.05	+
158	II	CC155	155	2013	meat	1/2a		-	-	0.04	+
167	II	CC155	155	2013	poultry	1/2c		-	-	0.05	+
184	II	CC155	155	2014	dryed meat	1/2a		-	-	0.04	+
203	II	CC155	155	2014	dryed meat	1/2a		-	-	0.14	+
224	II	CC155	155	2014	meat environment	1/2a		-	-	0.13	+
27	II	CC177	740	2011	milk	1/2a		-	-	0.11	-

66	II	CC199	230	2012	milk	1/2a		-	-	0.09	+
70	II	CC199	230	2012	milk	1/2a		-	-	0.11	+
71	II	CC199	230	2012	cheese crust	1/2a		-	-	0.09	+
20	II	CC204	204	2011	meat	1/2a		-	-	0.22	+
37	II	CC204	204	2012	quorn	1/2a		-	-	0.06	+
62	II	CC204	204	2012	meat	1/2a		-	-	0.10	+
110	II	CC204	204	2012	meat	1/2a		-	-	0.15	+
148	II	CC204	204	2013	scaleded sausage	1/2a		-	-	0.07	+
149	II	CC204	204	2013	meat	1/2a		-	-	0.00	+
150	II	CC204	204	2013	meat	1/2a		-	-	0.03	+
177	II	ST226	226	2014	cooked vegetables	1/2a		-	-	0.06	+
171	II	ST307	307	2013	butter	1/2a		-	-	0.20	nd
13	II	CC361	415	2011	meat	1/2a		-	-	0.05	-
17	II	CC361	415	2011	meat	1/2a		-	-	0.10	-
131	II	CC361	415	2013	meat	1/2a		-	-	0.03	-
32	II	CC361	744	2012	cheese environment	1/2a		-	-	0.02	-
153	II	ST375	375	2013	salad	1/2a		-	-	0.11	+
29	II	CC403	738	2011	meat	1/2a		-	-	0.13	nd[c]
137	II	CC451	451	2013	poultry	1/2a		-	-	0.07	nd
30	II	CC451	733	2012	meat	1/2a		-	-	0.06	-
40	II	CC504	504	2012	shrimp	1/2a		-	-	0.06	*
44	II	CC504	504	2012	shrimp	1/2a		-	-	0.03	*
46	II	CC504	504	2012	shrimp	1/2a		-	-	0.07	*
212	II	CC504	504	2014	seafood	1/2a	20	-	-	0.04	*

28	II	ST739	739	2011	cheese	1/2a		-	-	0.17	+
133	II	ST749	749	2013	meat	1/2a	25	+	-	0.20	*

[a] highest tolerated concentration where growth was determined

[b] *, band at a different length (2.2 kbp) than expected

[c] nd, not detected

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